FIG. 1A-1

```
  1  GTCGACCCAC GCGTCCGAGA AGAAAACCCT AGATTTCTCC GTCTCTCTAA TTTCCTTTCT

 61  CTCTCAAGCT TCTCAGAAAG TCTGACACTT TCGAGAATCT AATCTCCAAA TTTCTTGTCT

121  TTTTGGAGAA GGAATCGAAT T ATG TAC AAG GAA CGT AGT GGA GGA GGT GGT GGT GGG TCA
                            Met Tyr Lys Glu Arg Ser Gly Gly Gly Gly Gly Gly Ser      13

181  TCG AGA TCA GAG ATC CTC GGT GGA GCT ATT GAT CGG AAA CGA ATC AAC GAT GCA CTC AAT
     Ser Arg Ser Glu Ile Leu Gly Gly Ala Ile Asp Arg Lys Arg Ile Asn Asp Ala Leu Asn    33

241  AAG AAA CTA GAG AAA TCT TCA ACT TCC ACC ACC ACA TCT AGG GTT TTC TCT TCT AAA GAC
     Lys Lys Leu Glu Lys Ser Ser Thr Ser Thr Thr Thr Ser Arg Val Phe Ser Ser Lys Asp    53

301  AAA GAT CCC TTT TCC TTC ACA TCT ACT AAA ACT CAG CTT CCT GAT GTG GAA TCG GAA ACT
     Lys Asp Pro Phe Ser Phe Thr Ser Thr Lys Thr Gln Leu Pro Asp Val Glu Ser Glu Thr    73

361  GAT AGT GAA GGG TCT GAT GTG AGT GGA TCG GAG GGT GAT GAT ACG TCG TGG ATC TCT TGG
     Asp Ser Glu Gly Ser Asp Val Ser Gly Ser Glu Gly Asp Asp Thr Ser Trp Ile Ser Trp    93

421  TTT TGT AAT TTG AGA GGG AAT GAT TTC TTC TGT GAA GTC GAT GAA GAT TAT ATT CAA GAT
     Phe Cys Asn Leu Arg Gly Asn Asp Phe Phe Cys Glu Val Asp Glu Asp Tyr Ile Gln Asp   113

481  GAT TTC AAT CTT TGT GGT TTA AGT GGT CAA GTC CCT TAC TAT GAT TAT GCA CTT GAT CTC
     Asp Phe Asn Leu Cys Gly Leu Ser Gly Gln Val Pro Tyr Tyr Asp tyr Ala Leu Asp Leu   133

541  ATT TTA GAT GTT GAT GCT TCC AAC AGT GAG ATG TTT ACT GAT GAA CAG CAT GAA ATG GTG
     Ile Leu Asp Val Asp Ala Ser Asn Ser Glu Met Phe Thr Asp Glu Gln His Glu Met Val   153
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FIG. 1A-2

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601  GAA TCA GCT GCT GAG ATG CTA TAT GGT CTT ATT CAT GTT CGT TAC ATT TTG ACT ACT AAA
     Glu Ser Ala Ala Glu Met Leu Tyr Gly Leu Ile His Val Arg Tyr Ile Leu Thr Thr Lys   173

661  GGA ATG GCT GCA ATG ACT GAG AAG TAC AAG AAC TGT GAT TTC GGG AGA TGC CCG AGA GTT
     Gly Met Ala Ala Met Thr Glu Lys Tyr Lys Asn Cys Asp Phe Gly Arg Cys Pro Arg Val   193

721  TTC TGT TGC GGT CAG TCT TGT CTT CCA GTT GGA CAA TCC GAT ATC CCG AGA TCG AGT ACT
     Phe Cys Cys Gly Gln Ser Cys Leu Pro Val Gly Gln Ser Asp Ile Pro Arg Ser Ser Thr   213

781  GTG AAG ATA TAC TGC CCT AAA TGC GAG GAT ATA TCT TAC CCG CGA TCT AAA TTC CAA GGC
     Val Lys Ile Tyr Cys Pro Lys Cys Glu Asp Ile Ser Tyr Pro Arg Ser Lys Phe Gln Gly   233

841  AAT ATT GAT GGA GCG TAC TTT GGA ACC ACA TTC CCT CAC TTG TTC TTG ATG ACT TAC GGG
     Asn Ile Asp Gly Ala Tyr Phe Gly Thr Thr Phe Pro His Leu Phe Leu Met Thr Tyr Gly   253

901  AAC TTA AAG CCG CAG AAG CCT ACT CAA AGC TAT GTC CCA AAA ATC TTT GGC TTC AAG GTA
     Asn Leu Lys Pro Gln Lys Pro Thr Gln Ser Tyr Val Pro Lys Ile Phe Gly Phe Lys Val   273

960  CAC AAA CCA TGATACTAGT GCTCTGCATT CTCAATGGTG ATACATTTAG TGGCTCTGTA
     His Lys Pro                                                                     276

1020 ATTGCATCCG GATGAGCAAC TGAAACGATA GCTGCGGTGA CTGGAGCATA CATCAACCAT T
```

FIG. 1B

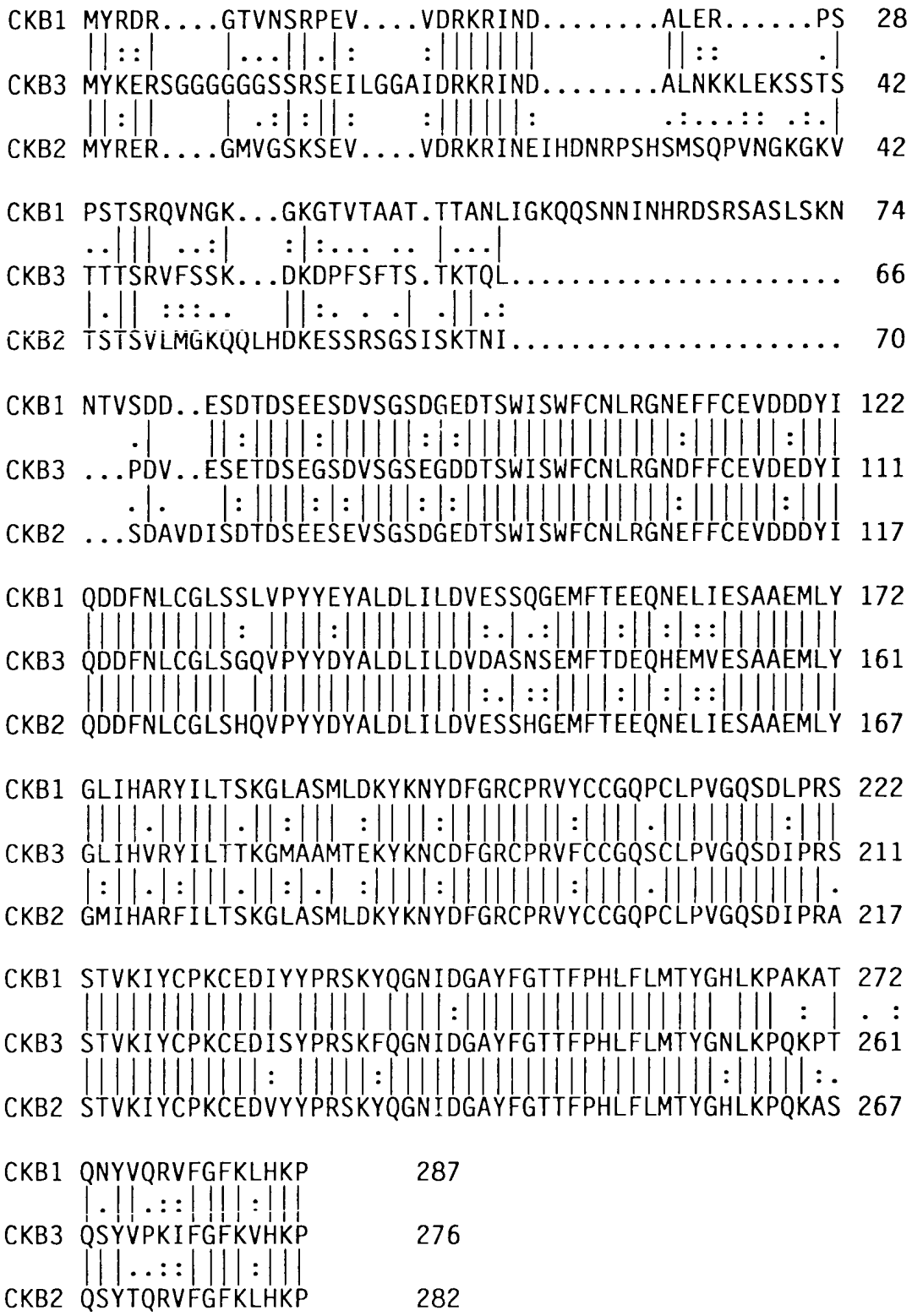


FIG. 2

SEQ. I.D. No.1

GTCGACCCAC GCGTCCGAGA AGAAAACCCT AGATTTCTCC GTCTCTCTAA TTTCCTTTCT 60

CTCTCAAGCT TCTCAGAAAG TCTGACACTT TCGAGAATCT AATCTCCAAA TTTCTTGTCT 120

TTTTGGAGAA GGAATCGAAT TATGTACAAG GAACGTAGTG GAGGAGGTGG TGGTGGGTCA 180

TCGAGATCAG AGATCCTCGG TGGAGCTATT GATCGGAAAC GAATCAACGA TGCACTCAAT 240

AAGAAACTAG AGAAATCTTC AACTTCCACC ACCACATCTA GGGTTTTCTC TTCTAAAGAC 300

AAAGATCCCT TTTCCTTCAC ATCTACTAAA ACTCAGCTTC CTGATGTGGA ATCGGAAACT 360

GATAGTGAAG GGTCTGATGT GAGTGGATCG GAGGGTGATG ATACGTCGTG GATCTCTTGG 420

TTTTGTAATT TGAGAGGGAA TGATTTCTTC TGTGAAGTCG ATGAAGATTA TATTCAAGAT 480

GATTTCAATC TTTGTGGTTT AAGTGGTCAA GTCCCTTACT ATGATTATGC ACTTGATCTC 540

ATTTTAGATG TTGATGCTTC CAACAGTGAG ATGTTTACTG ATGAACAGCA TGAAATGGTG 600

GAATCAGCTG CTGAGATGCT ATATGGTCTT ATTCATGTTC GTTACATTTT GACTACTAAA 660

GGAATGGCTG CAATGACTGA GAAGTACAAG AACTGTGATT TCGGGAGATG CCCGAGAGTT 720

TTCTGTTGCG GTCAGTCTTG TCTTCCAGTT GGACAATCCG ATATCCCGAG ATCGAGTACT 780

GTGAAGATAT ACTGCCCTAA ATGCGAGGAT ATATCTTACC CGCGATCTAA ATTCCAAGGC 841

AATATTGATG GAGCGTACTT TGGAACCACA TTCCCTCACT TGTTCTTGAT GACTTACGGG 900

AACTTAAAGC CGCAGAAGCC TACTCAAAGC TATGTCCCAA AAATCTTTGG CTTCAAGGTA 961

CACAAACCAT GATACTAGTG CTCTGCATTC TCAATGGTGA TACATTTAGT GGCTCTGTAA 1020

TTGCATCCGG ATGAGCAACT GAAACGATAG CTGCGGTGAC TGGAGCATAC ATCAACCATT 1080

FIG. 3

SEQ. I.D. No.2

Met Tyr Lys Glu Arg Ser Gly Gly Gly Gly Gly Gly Ser Ser Arg Ser Glu Ile Leu Gly 20

Gly Ala Ile Asp Arg Lys Arg Ile Asn Asp Ala Leu Asn Lys Lys Leu Glu Lys Ser Ser 40

Thr Ser Thr Thr Thr Ser Arg Val Phe Ser Ser Lys Asp Lys Asp Pro Phe Ser Phe Thr 60

Ser Thr Lys Thr Gln Leu Pro Asp Val Glu Ser Glu Thr Asp Ser Glu Gly Ser Asp Val 80

Ser Gly Ser Glu Gly Asp Asp Thr Ser Trp Ile Ser Trp Phe Cys Asn Leu Arg Gly Asn 100

Asp Phe Phe Cys Glu Val Asp Glu Asp Tyr Ile Gln Asp Asp Phe Asn Leu Cys Gly Leu 120

Ser Gly Gln Val Pro Tyr Tyr Asp Tyr Ala Leu Asp Leu Ile Leu Asp Val Asp Ala Ser 140

Asn Ser Glu Met Phe Thr Asp Glu Gln His Glu Met Val Glu Ser Ala Ala Glu Met Leu 160

Tyr Gly Leu Ile His Val Arg Tyr Ile Leu Thr Thr Lys Gly Met Ala Ala Met Thr Glu 180

Lys Tyr Lys Asn Cys Asp Phe Gly Arg Cys Pro Arg Val Phe Cys Cys Gly Gln Ser Cys 200

Leu Pro Val Gly Gln Ser Asp Ile Pro Arg Ser Ser Thr Val Lys Ile Tyr Cys Pro Lys 220

Cys Glu Asp Ile Ser Tyr Pro Arg Ser Lys Phe Gln Gly Asn Ile Asp Gly Ala Tyr Phe 240

Gly Thr Thr Phe Pro His Leu Phe Leu Met Thr Tyr Gly Asn Leu Lys Pro Gln Lys Pro 260

Thr Gln Ser Tyr Val Pro Lys Ile Phe Gly Phe Lys Val His Lys Pro 276

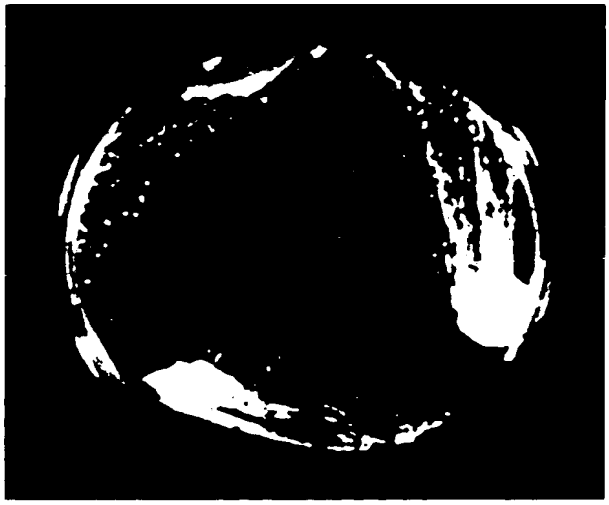
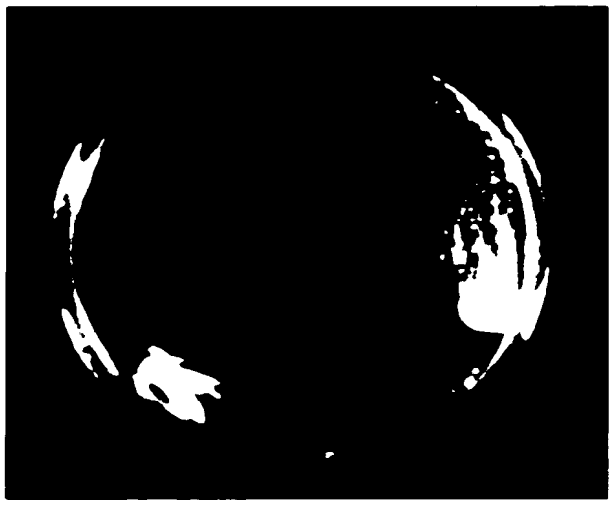


FIG. 4

35.5 °C

pKT10

pJCR14



pKT-CKB3

FIG. 5A

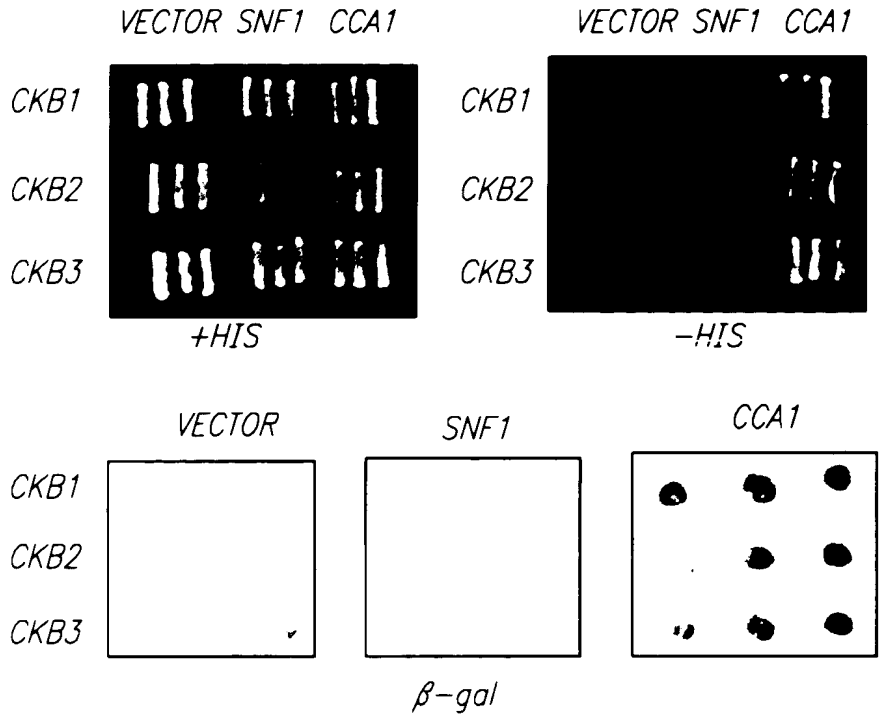
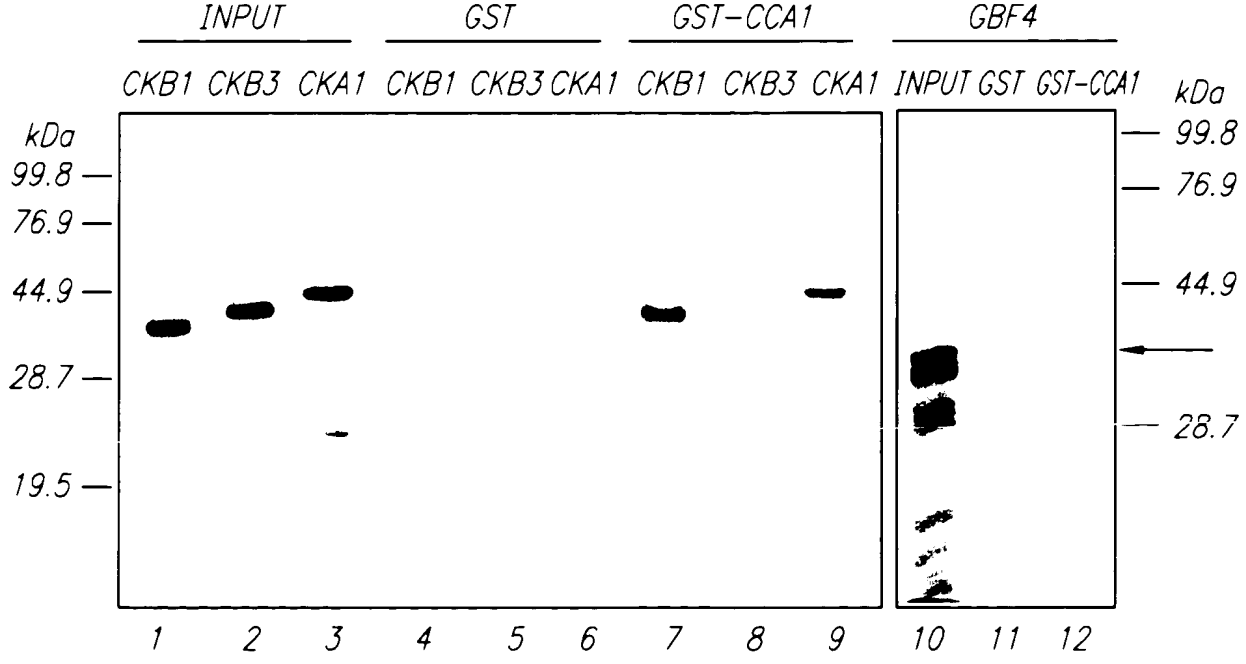


FIG. 5B



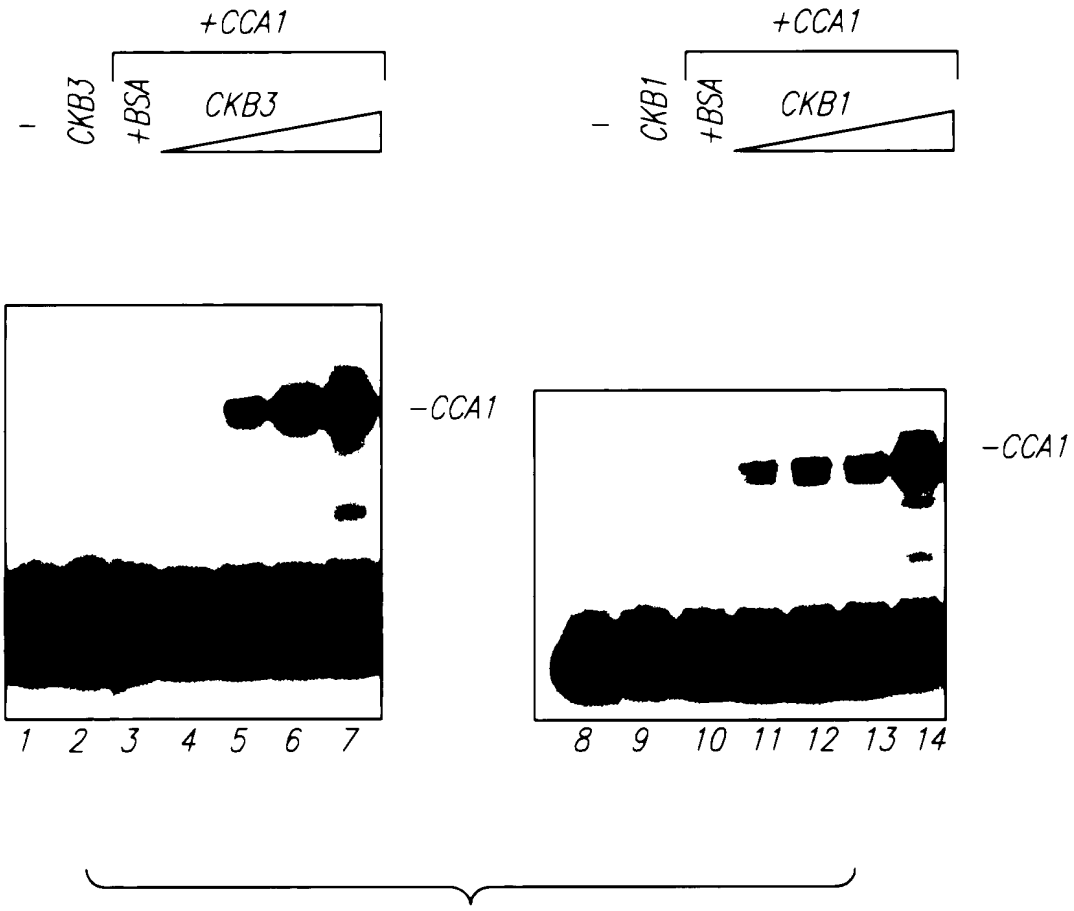


FIG. 6

FIG. 7A

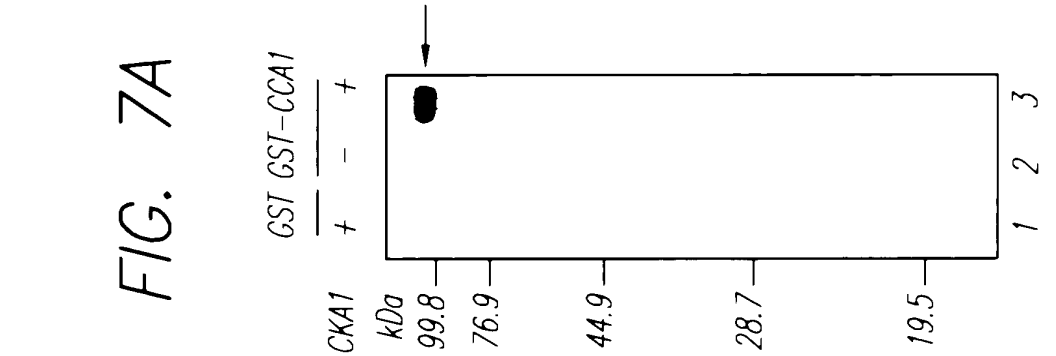


FIG. 7B

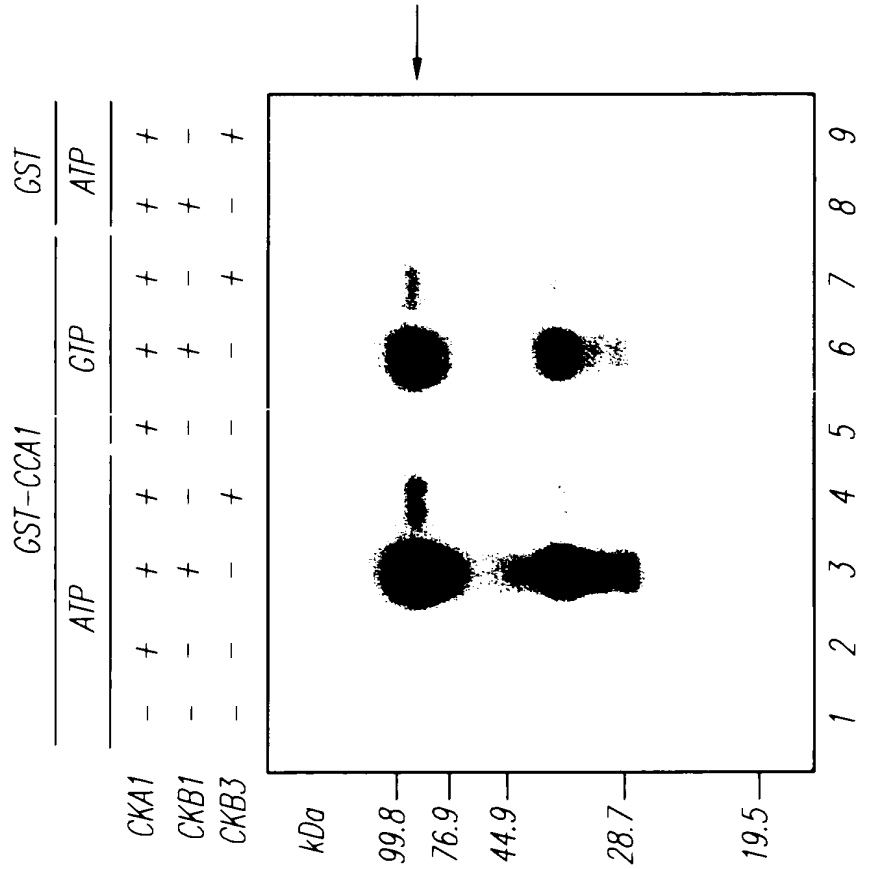
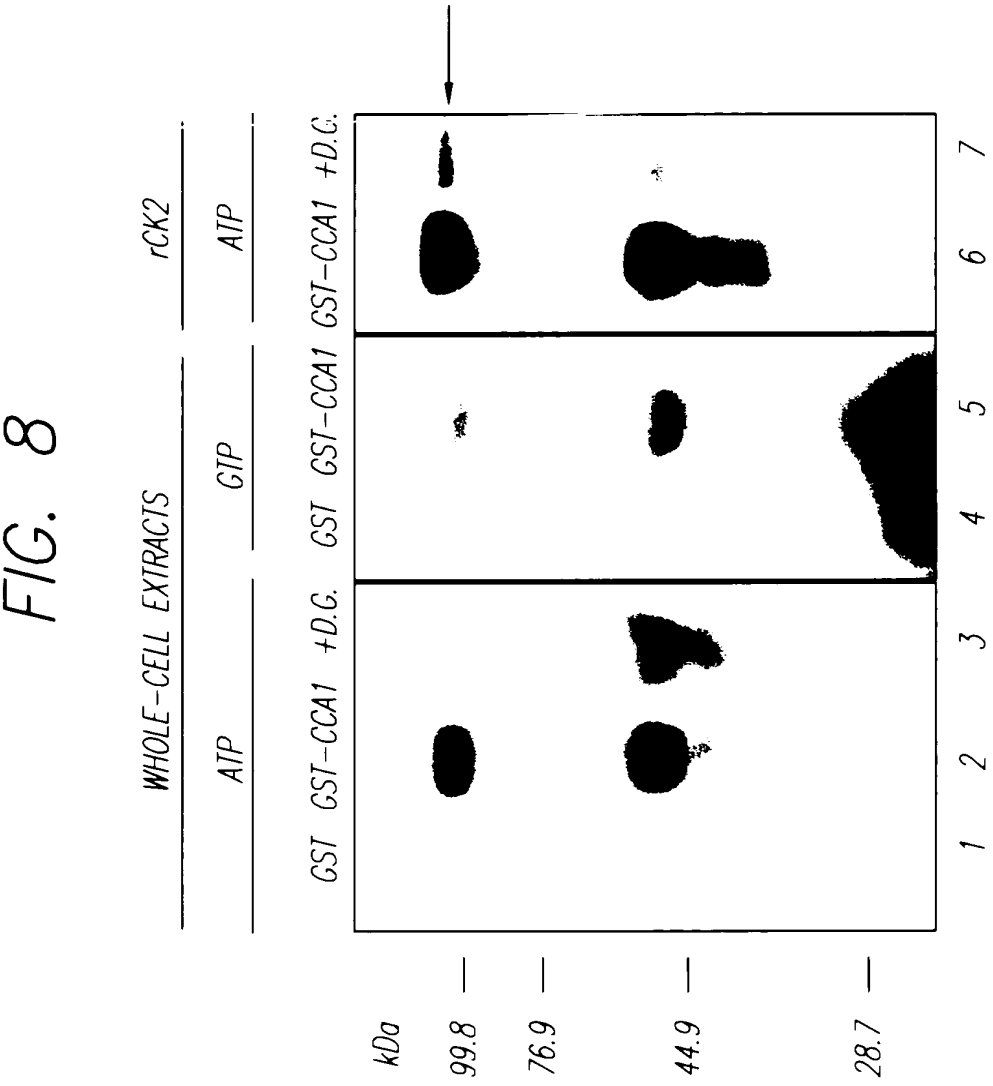


FIG. 8



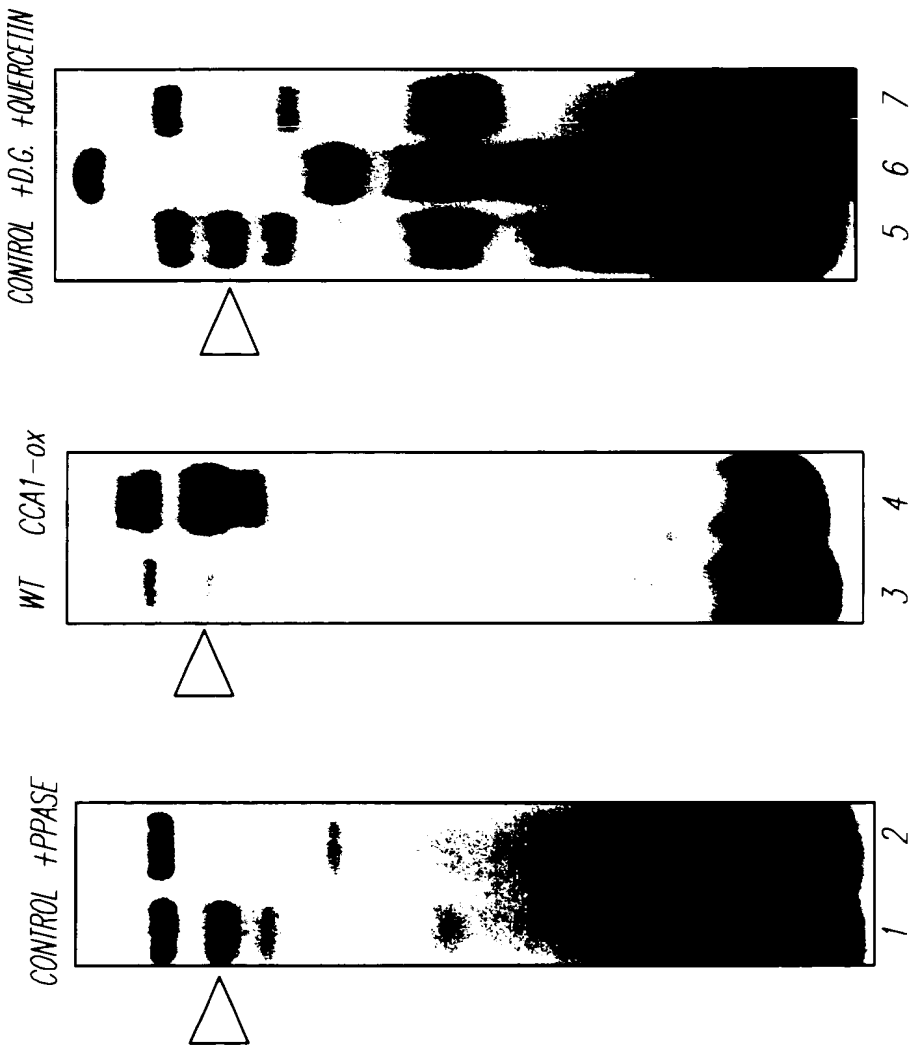


FIG. 9A FIG. 9B FIG. 9C

FIG. 10A

FIG. 10B

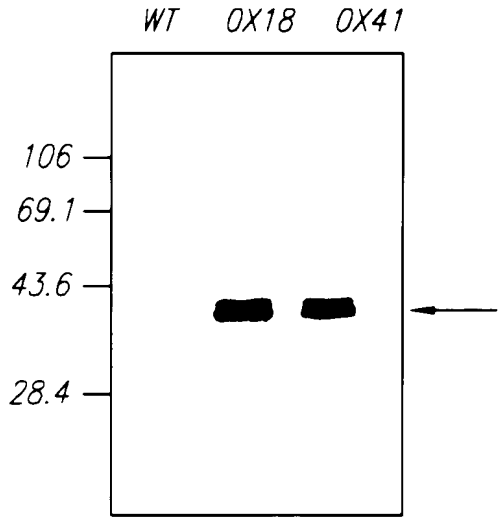
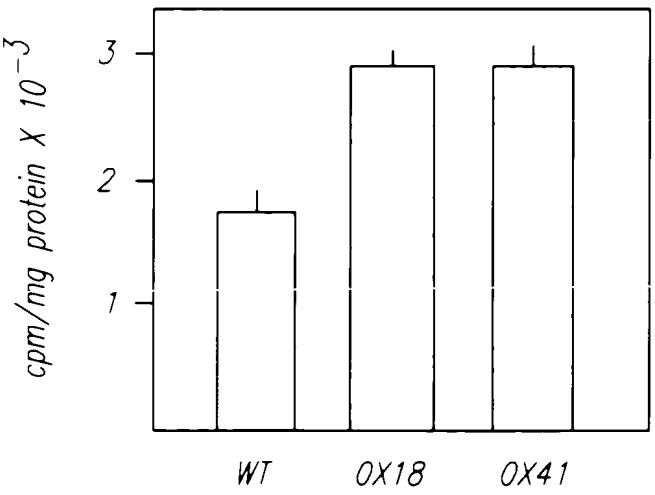


FIG. 10C



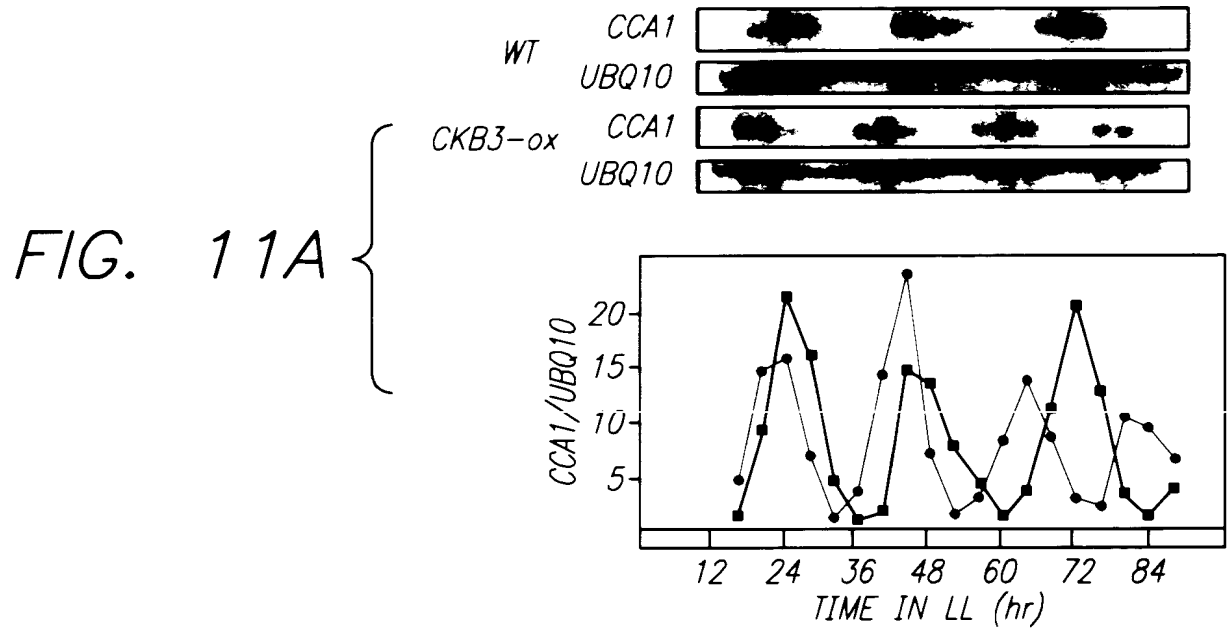


FIG. 11A

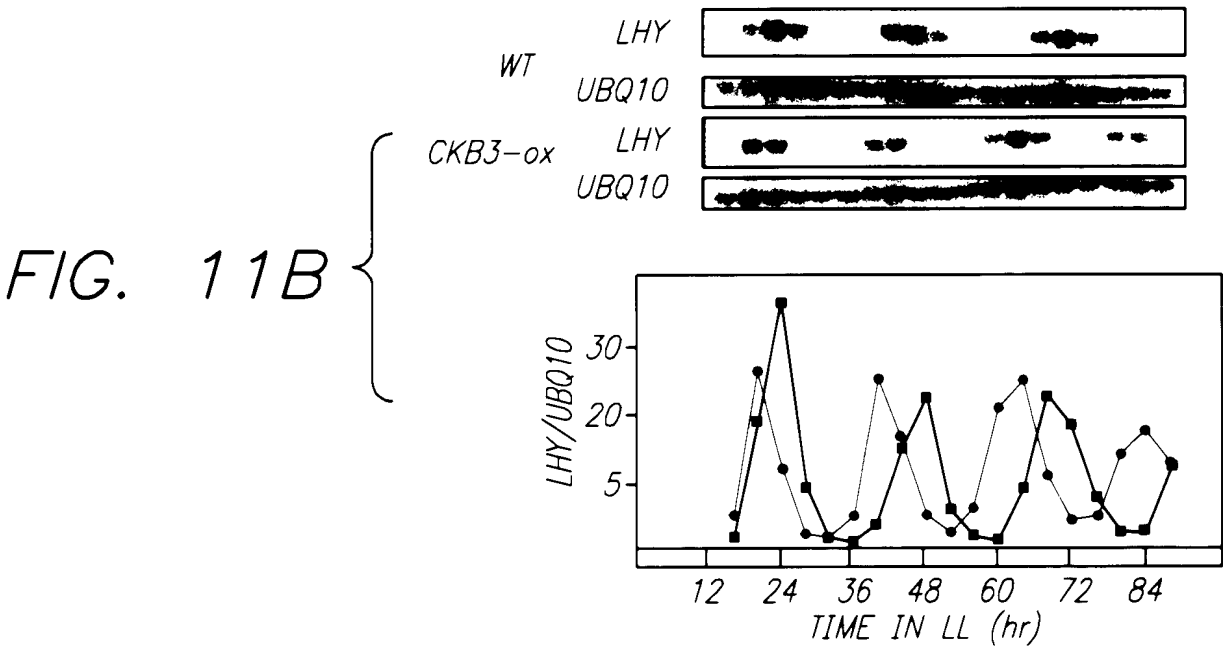


FIG. 11B

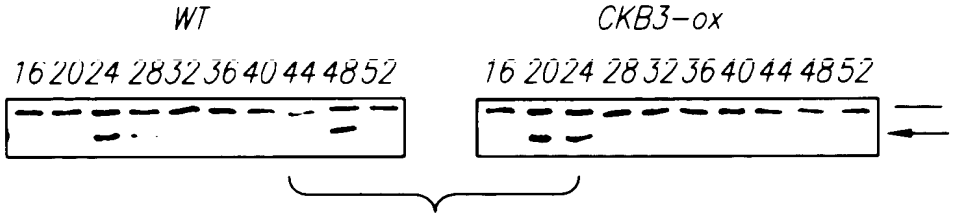


FIG. 11C

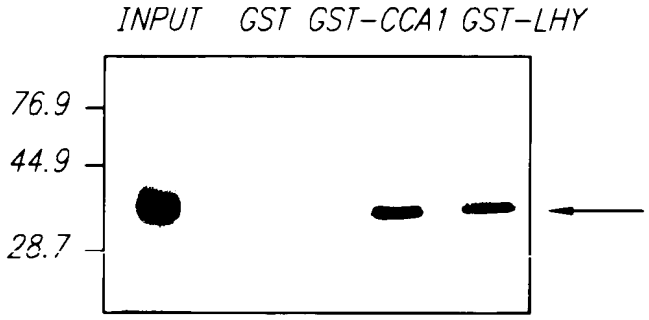


FIG. 12A

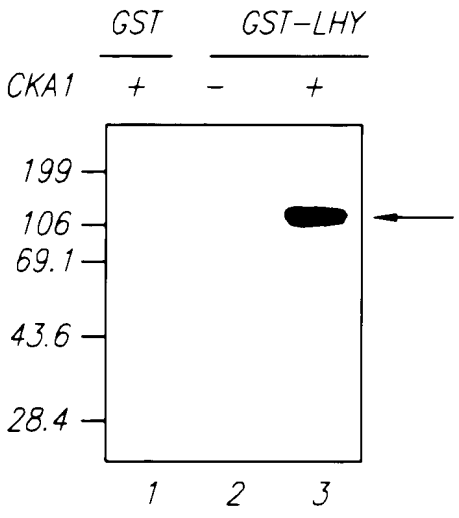


FIG. 12B

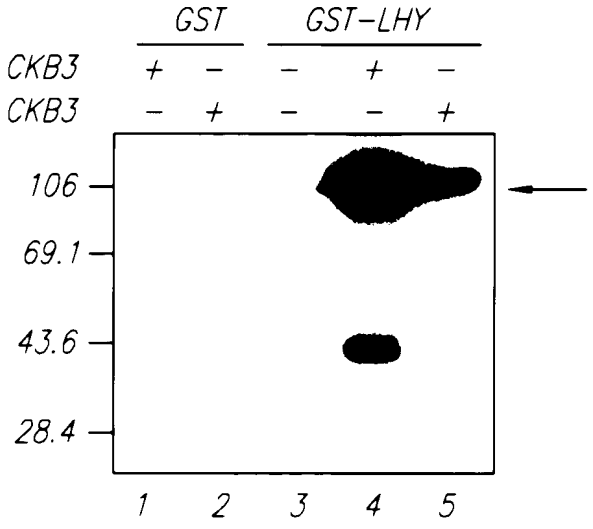


FIG. 12C

FIG. 13A

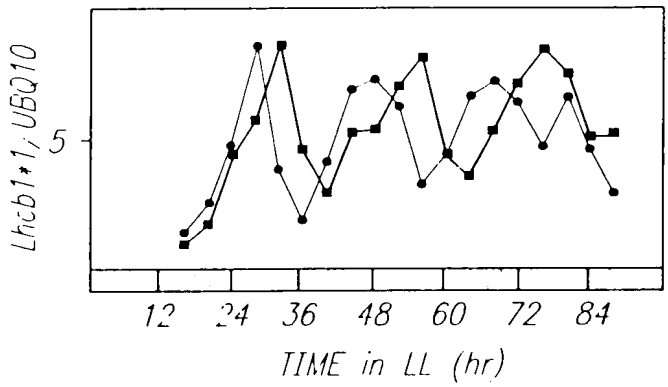


FIG. 13B

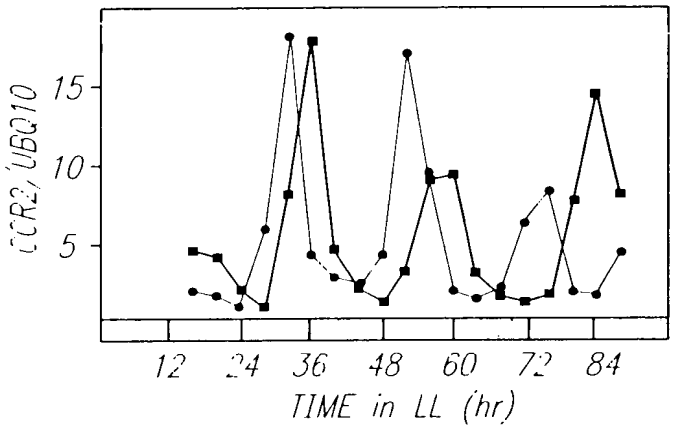


FIG. 13C

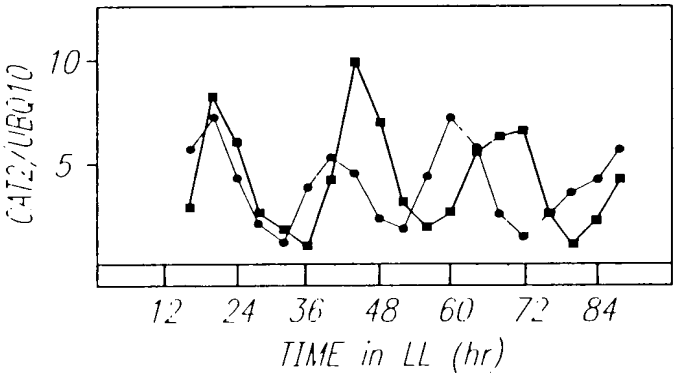


FIG. 13D